

RAW SEQUENCE LISTING

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Application Serial Number: 10/521,138
Source: PG
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/521,138

DATE: 04/14/2006

TIME: 11:20:54

Input Set : A:\-159-2.APP

Output Set: N:\CRF4\04142006\J521138.raw

3 <110> APPLICANT: Johnson, Karl F.
 4 Bezila, Daniel James
 5 Taylor, Diane E.
 6 Simala-Grant, Joanne
 7 Rasko, David
 8 Neose Technologies, Inc.
 9 Governors of the University of Alberta
 11 <120> TITLE OF INVENTION: Synthesis of Oligosaccharides, Glycolipids and
 12 Glycoproteins Using Bacterial Glycosyltransferases
 14 <130> FILE REFERENCE: 019957-015920US
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/521,138
 C--> 17 <141> CURRENT FILING DATE: 2005-01-12
 19 <150> PRIOR APPLICATION NUMBER: US 60/398,156
 20 <151> PRIOR FILING DATE: 2002-07-23
 22 <150> PRIOR APPLICATION NUMBER: US 60/424,894
 23 <151> PRIOR FILING DATE: 2002-11-08
 25 <150> PRIOR APPLICATION NUMBER: WO PCT/US03/23057
 26 <151> PRIOR FILING DATE: 2003-07-23
 28 <150> PRIOR APPLICATION NUMBER: WO PCT/US03/23155
 29 <151> PRIOR FILING DATE: 2003-07-23
 31 <160> NUMBER OF SEQ ID NOS: 76
 33 <170> SOFTWARE: PatentIn Ver. 2.1
 35 <210> SEQ ID NO: 1
 36 <211> LENGTH: 1461
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Helicobacter pylori
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: Helicobacter pylori strain 1182 FutB
 42 alpha-1,3/4-fucosyltransferase
 44 <400> SEQUENCE: 1
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 46 aaatctcccc cccccctaaa aatcgctgtg gcgaatttgtt ggggagatga agaggttgaa 120
 47 gaatttaaaa agaacattct ttatTTTATT ctcagtcagc attacacaat caccctccac 180
 48 caaaacccca acgaaccctc cgatctcgtc tttggcagtc ctattggatc agccagaaaa 240
 49 atcttatacct atcaaaacgc aaaaagagtgt ttttacacccg gtgaaaacga atcgccataat 300
 50 ttcaacctct ttgattacgc cataggctt gatgaattgg attttagaga tcgttattta 360
 51 agaatgcctt tatattatga tagactacac cataaagccg agagcgtgaa tgacaccact 420
 52 tcgccttaca aactcaaacc tgacagcctt tatgctttaa aaaaaccctc ccatcatttt 480
 53 aaagaaaaacc accccaattt atgcgcagta gtgaacaatg agagcgatcc tttgaaaaga 540
 54 gggtttgcga gttttgttagc gagcaaccct aacgctccta aaaggaatgc tttctatgac 600
 55 gtttaaatt ctatagagcc agttattggg ggagggagcg tgaaaaacac tttaggctat 660
 56 aacattaaaa acaagagcga gttttaagc caatacaaat tcaatctgtg ttttgaaaac 720
 57 tcacaaggct atggctatgt aactgaaaaa atcattgacg cttactttag ccataccatt 780

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 60 ccaaacgcctt attagacat gctttatgaa aaccctttaa acacccttga tggaaaagct 960
 61 tacttttacc aaaatttgag tttaaaaaa atcctagatt tttttaaaac gattttagaa 1020
 62 aacgacacga tttatcacga taaccctttt atttttatc gtgatttggaa tgagccgtta 1080
 63 atatctattg atgatgattt gagggttaat tatgatgatt tgagggttaa ttatgatgat 1140
 64 ttgagggtta attatgatga tttgagggtt aattatgatg atttgagggt taattatgat 1200
 65 gatttgaggg ttaattatga tgatttgagg gtttaattatg atgatttgag gtttaattat 1260
 66 gatgatttga gggtaatta tgatgattt agggtaattt atgatgattt gagggttaat 1320
 67 tatgagcggc tcttacaaaa cgcctcgcc ttattagaac tctctcaaaa caccacttt 1380
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 88 Trp Trp Gly Asp Glu Glu Val Glu Phe Lys Lys Asn Ile Leu Tyr
 89 35 40 45
 91 Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn
 92 50 55 60
 94 Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys
 95 65 70 75 80
 97 Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn
 98 85 90 95
 100 Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
 101 100 105 110
 103 Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg
 104 115 120 125
 106 Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys
 107 130 135 140
 109 Leu Lys Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe
 110 145 150 155 160
 112 Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp
 113 165 170 175
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 116 180 185 190
 118 Pro Lys Arg Asn Ala Phe Tyr Asp Val Leu Asn Ser Ile Glu Pro Val
 119 195 200 205
 121 Ile Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn
 122 210 215 220
 124 Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn

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128	245	250	255	
130	Ser His Thr Ile Pro Ile Tyr Trp Gly Ser Pro Ser Val Ala Gln Asp			
131	260	265	270	
133	Phe Asn Pro Lys Ser Phe Val Asn Val Cys Asp Phe Lys Asp Phe Asp			
134	275	280	285	
136	Glu Ala Ile Asp His Val Arg Tyr Leu His Thr His Pro Asn Ala Tyr			
137	290	295	300	
139	Leu Asp Met Leu Tyr Glu Asn Pro Leu Asn Thr Leu Asp Gly Lys Ala			
140	305	310	315	320
142	Tyr Phe Tyr Gln Asn Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys			
143	325	330	335	
145	Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Asp Asn Pro Phe Ile Phe			
146	340	345	350	
148	Tyr Arg Asp Leu Asn Glu Pro Leu Ile Ser Ile Asp Asp Asp Leu Arg			
149	355	360	365	
151	Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn			
152	370	375	380	
154	Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp			
155	385	390	395	400
157	Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu			
158	405	410	415	
160	Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val			
161	420	425	430	
163	Asn Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala			
164	435	440	445	
166	Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys Ile Tyr Arg			
167	450	455	460	
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178	<212> TYPE: DNA			
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181	<220> FEATURE:			
182	<223> OTHER INFORMATION: Helicobacter pylori strain 1111 Futa			
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188	tttaaaaaga gcgttctta ttttatccta agccagcatt acacaatcac ttacaccga 180			
189	aacctctgata aacctgcgga catcgtctt ggtaacccc ttggatcagc cagaaaaatc 240			
190	ttatcctatc aaaacgcaa aagggtgtt tacaccggtg aaaatgaagt ccctaacttc 300			
191	aacctctttg attacgccat aggcttgcat gaattggact tttagagatcg ttatggaga 360			
192	atgcctttgt attatgccta ttgcattat aaagccgagc ttgttaatga caccacttcg 420			
193	ccttataaac tccaaacctga cagcctttat gctttaaaaa aaccctccca tcattttaaa 480			

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194 gaaaaccacc ccaatttgcg cgcaagtatgt aataatgaga gtgatccttt gaaaagaggg 540
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 196 ttaaacgccta ttgagccagt tgctggggga gggagcgtga aaaacactt aggctataat 660
 197 gtcaaaaaca agagcgagtt ttaagccaa tacaaattca atctgtgtt tgaaaacact 720
 198 caaggctatg gctatgtaac tgaaaagatc attgacgctt attcagcca taccattcct 780
 199 atttatttggg ggagtcccag cgtggcgaaa gatttaacc ctaagagtt ttgtaatgtc 840
 200 catgatttca acaacttga tgaagcgatt gactatatca gatacttgcac cacgcaccca 900
 201 aacgcttatt tagacatgca ctatgaaaac cctttaaaca ctattgtgg gaaagcttac 960
 202 ttttacccaa attttagttt taaaaaaaaatc ctagattttt ttaaaacatgat ttttagaaaac 1020
 203 gacacgatct atcacgataa ccctttcatt ttctatcgat atttgaatgac gccttcgat 1080
 204 tctattgtatg gtttgagggt taatttatgat gatttgagggt ttaattatgat tgatttgagg 1140
 205 gtaattatg atgatttgag gtttaattat gagcgcctt tacaacacgc ctcgcctta 1200
 206 tttagaactct ctcaaaacac cactttaaa atctatcgat aagcttatca aaaatccttg 1260
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 217 alpha-1,3/4-fucosyltransferase
 219 <400> SEQUENCE: 4
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 224 20 25 30
 226 Trp Gly Asp Glu Glu Ile Lys Lys Phe Lys Lys Ser Val Leu Tyr Phe
 227 35 40 45
 229 Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Arg Asn Pro Asp Lys
 230 50 55 60
 232 Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg Lys Ile
 233 65 70 75 80
 235 Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu
 236 85 90 95
 238 Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu
 239 100 105 110
 241 Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala Tyr Leu
 242 115 120 125
 244 His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu
 245 130 135 140
 247 Gln Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys
 248 145 150 155 160
 250 Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro
 251 165 170 175
 253 Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro
 254 180 185 190
 256 Arg Arg Asn Ala Phe Tyr Glu Ala Leu Asn Ala Ile Glu Pro Val Ala
 257 195 200 205
 259 Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Val Lys Asn Lys

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265	Gln	Gly	Tyr	Gly	Tyr	Val	Thr	Glu	Lys	Ile	Ile	Asp	Ala	Tyr	Phe	Ser
266										245		250				255
268	His	Thr	Ile	Pro	Ile	Tyr	Trp	Gly	Ser	Pro	Ser	Val	Ala	Lys	Asp	Phe
269									260		265				270	
271	Asn	Pro	Lys	Ser	Phe	Val	Asn	Val	His	Asp	Phe	Asn	Asn	Phe	Asp	Glu
272									275		280				285	
274	Ala	Ile	Asp	Tyr	Ile	Arg	Tyr	Leu	His	Thr	His	Pro	Asn	Ala	Tyr	Leu
275								290		295				300		
277	Asp	Met	His	Tyr	Glu	Asn	Pro	Leu	Asn	Thr	Ile	Asp	Gly	Lys	Ala	Tyr
278	305							310			315				320	
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281								325			330				335	
283	Ile	Leu	Glu	Asn	Asp	Thr	Ile	Tyr	His	Asp	Asn	Pro	Phe	Ile	Phe	Tyr
284								340			345				350	
286	Arg	Asp	Leu	Asn	Glu	Pro	Ser	Val	Ser	Ile	Asp	Gly	Leu	Arg	Val	Asn
287								355			360				365	
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290								370			375				380	
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293	385							390			395				400	
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296								405			410				415	
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302 <210> SEQ ID NO: 5

303 <211> LENGTH: 1458

304 <212> TYPE: DNA

305 <213> ORGANISM: Helicobacter pylori

307 <220> FEATURE:

308 <223> OTHER INFORMATION: Helicobacter pylori strain 1218 FutB

309 alpha-1,3/4-fucosyltransferase

311 <400> SEQUENCE: 5

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VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application Number

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date